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Cys Leu Lys Asp Ile Thr Asp Phe Glu Phe Pro Gln Glu Ile Leu Leu 50 55

Tyr Val Gln His Val Lys Lys Asp Ile Lys Ala Val Thr Tyr His Ile
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Ser Ser Leu Ala Leu Ile Ile Phe Ser Leu Lys Asp Ser Ile Ser Leu 85 90 95

Ala Thr Glu Glu Arg Leu Glu Arg Ile Arg Ser Gly Leu Phe Lys Gln
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Val Gln Gln Ala Arg Glu Cys Met Val Asp Glu Glu Asn Lys Asn Thr 115 120 125

Glu Glu Asp Ser Thr Ser Gln His Pro His Ser Glu Gly Phe Lys Ala 130 135 140

Val Tyr Leu Glu Leu Asn Lys Tyr Phe Phe Arg Ile Arg Lys Phe Leu 145 150 155 160

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Ser Ile Arg Thr Thr Phe Pro Leu Arg Cys Leu Lys Asp Ile Thr Asp 20 25 30

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35 40 45

Asp Ile Lys Ala Val Thr Tyr His Ile Ser Ser Leu Ala Leu Ile Ile 50 55 60

Phe Ser Leu Lys Asp Ser Ile Ser Leu Ala Thr Glu Glu Arg Leu Glu 65 70 75 80

Arg Ile Arg Ser Gly Leu Phe Lys Gln Val Gln Gln Ala Arg Glu Cys 85 90 95

Met Val Asp Glu Glu Asn Lys Asn Thr Glu Glu Asp Ser Thr Ser Gln
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His Pro His Ser Glu Gly Phe Lys Ala Val Tyr Leu Glu Leu Asn Lys 115 120 125

Tyr Phe Phe Arg Ile Arg Lys Phe Leu Val Asn Lys Lys Tyr Ser Phe

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3

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gtc acc tgg caa aat ctg aga cat ctg agt agt atg agc aat tca ttt 739
Val Thr Trp Gln Asn Leu Arg His Leu Ser Ser Met Ser Asn Ser Phe
40 45 50 55

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Ser Ser Met Ser Asn Ser Phe Pro Val Glu Cys Leu Arg Glu Asn Ile 50 55 60

Ala Phe Glu Leu Pro Gln Glu Phe Leu Gln Tyr Thr Gln Pro Met Lys
65 70 75 80

Arg Asp Ile Lys Lys Ala Phe Tyr Glu Met Ser Leu Gln Ala Phe Asn 85 90 95

Ile Phe Ser Gln His Thr Phe Lys Tyr Trp Lys Glu Arg His Leu Lys
100 105 110

Gln Ile Gln Ile Gly Leu Asp Gln Gln Ala Glu Tyr Leu Asn Gln Cys 115 120 125

Leu Glu Glu Asp Glu Asn Glu Asp Met Lys Glu Met Lys Glu 130 135 140

Asn Glu Met Lys Pro Ser Glu Ala Arg Val Pro Gln Leu Ser Ser Leu 145 155 160

Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe Leu Lys Glu Lys 165 170 175

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<213> Homo sapiens

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Glu Asn Ile Ala Phe Glu Leu Pro Gln Glu Phe Leu Gln Tyr Thr Gln
35 40 45

Pro Met Lys Arg Asp Ile Lys Lys Ala Phe Tyr Glu Met Ser Leu Gln
50 60

Ala Phe Asn Ile Phe Ser Gln His Thr Phe Lys Tyr Trp Lys Glu Arg
65 70 75 80

His Leu Lys Gln Ile Gln Ile Gly Leu Asp Gln Gln Ala Glu Tyr Leu 85 90 95

Asn Gln Cys Leu Glu Glu Asp Glu Asn Glu Asn Glu Asp Met Lys Glu 100 105 110

Met Lys Glu Asn Glu Met Lys Pro Ser Glu Ala Arg Val Pro Gln Leu 115 120 125

Ser Ser Leu Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe Leu 130 135 140

Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val Glu 145 150 155 160

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Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg 35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu 50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile

the light light light light light light light light finite that the

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser

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Tyr	His	Gln 115	Ile	Asn	His	Leu	Lys 120	Thr	Val	Leu	Glu	Glu 125	Lys	Leu	Glu	
Lys	Glu 130	Asp	Phe	Thr	Arg	Gly 135		Leu	Met	Ser	Ser 140	Leu	His	Leu	Lys	
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His	Суз	Ala	Trp	Thr 165	Ile	Val	Arg	Val	Glu 170	Ile	Leu	Arg	Asn	Phe 175	Tyr	
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	agc Ser															96
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Asp	Phe	Glu 35	Phe	Pro	Gln	Glu	Ile 40	Leu	Leu	Tyr.	Val	Gln 45	His	Val	Lys	
Lys	Asp 50	Ile	Lys	Ala	Val	Thr 55	Tyr	His	Ile	Ser	Ser 60	Leu	Ala	Leu	Ile	
Ile	Phe	Ser	Leu	Lys	Asp	Ser	Ile	Ser	Leu	Ala	Thr	Glu	Glu	Arg	Leu	

Glu Arg Ile Arg Ser Gly Leu Phe Lys Gln Val Gln Gln Ala Arg Glu

Cys Met Val Asp Glu Glu Asn Lys Asn Thr Glu Glu Asp Ser Thr Ser

100 105 110 Gln His Pro His Ser Glu Gly Phe Lys Ala Val Tyr Leu Glu Leu Asn Lys Tyr Phe Phe Arg Ile Arg Lys Phe Leu Val Asn Lys Lys Tyr Ser 130 135 Phe Cys Ala Trp Lys Ile Val Val Glu Ile Arg Arg Cys Phe Ser 155 Ile Phe Tyr Lys Leu Leu Asn Met Asn 165

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<223> Description of Artificial Sequence: Rat IFN-like polypeptide cDNA insert and partial pAMG21 vector sequence

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acg gat ttt gag ttt cct caa gag att ctg ctg tac gtc cag cat gtg Thr Asp Phe Glu Phe Pro Gln Glu Ile Leu Leu Tyr Val Gln His Val

aaa aag gac atc aag gca gtc acc tat cat atc tct tct ctg gcg ctg Lys Lys Asp Ile Lys Ala Val Thr Tyr His Ile Ser Ser Leu Ala Leu

att att ttc agt ctt aaa gac tcc atc tcc ctg gcg aca gag gaa cgc 240 Ile Ile Phe Ser Leu Lys Asp Ser Ile Ser Leu Ala Thr Glu Glu Arg 70 75

ttg gaa cgt atc cgt tct ggt ctt ttc aaa caa gtg cag caa gct cgt 288 Leu Glu Arg Ile Arg Ser Gly Leu Phe Lys Gln Val Gln Gln Ala Arg 80 85

Glu Cys Met Val Asp Glu Glu Asn Lys Asn Thr Glu Glu Asp Ser Thr 100 110

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Суя	Met	Val	Asp 100	Glu	Glu	Asn	Lys	Asn 105	Thr	Glu	Glu		Ser 110	Thr	Ser	
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<220>

<223> Description of Artificial Sequence: Human IFN-like polypeptide cDNA insert and partial pAMG21 vector sequence

<220>

<221> CDS

<222> (22)..(558)

<400> 12

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ttt cct gta gaa tgt cta cga gaa aac ata gct ttt gag ttg ccc caa 147 Phe Pro Val Glu Cys Leu Arg Glu Asn Ile Ala Phe Glu Leu Pro Gln

gag ttt ctg caa tac acc caa cct atg aag agg gac atc aag aag gcc 195 Glu Phe Leu Gln Tyr Thr Gln Pro Met Lys Arg Asp Ile Lys Lys Ala

tto tat gaa atg too cta cag goo tto aac atc tto ago caa cac acc 243 Phe Tyr Glu Met Ser Leu Gln Ala Phe Asn Ile Phe Ser Gln His Thr 65

ttc aaa tat tgg aaa gag aga cac ctc aaa caa atc caa ata gga ctt Phe Lys Tyr Trp Lys Glu Arg His Leu Lys Gln Ile Gln Ile Gly Leu 75 80 85

gat cag caa gca gag tac ctg aac caa tgc ttg gag gaa gac gag aat Asp Gln Gln Ala Glu Tyr Leu Asn Gln Cys Leu Glu Glu Asp Glu Asn 95 105

gaa aat gaa gac atg aaa gaa atg aaa gag aat gag atg aaa ccc tca Glu Asn Glu Asp Met Lys Glu Met Lys Glu Asn Glu Met Lys Pro Ser 110 115 120

gaa gcc agg gtc ccc cag ctg agc agc ctg gaa ctg agg aga tat ttc 435 Glu Ala Arg Val Pro Gln Leu Ser Ser Leu Glu Leu Arg Arg Tyr Phe 125 130

cac agg ata gac aat ttc ctg aaa gaa aag aaa tac agt gac tgt gcc 483 His Arg Ile Asp Asn Phe Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala 145 tgg gag att gtc cga gtg gaa atc cgt cgt tgc ctg tac tac tit tac Trp Glu Ile Val Arg Val Glu Ile Arg Arg Cys Leu Tyr Tyr Phe Tyr 155 160 165 aaa ttt acc gct ctg ttc cgt cgt aaa taatggatcc 568 Lys Phe Thr Ala Leu Phe Arg Arg Lys 175 <210> 13 <211> 179 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Rat IFN-like polypeptide cDNA insert and partial pAMG21 vector sequence <400> 13 Met Cys Asn Leu Leu Asn Val His Leu Arg Arg Val Thr Trp Gln Asn 5 Leu Arg His Leu Ser Ser Met Ser Asn Ser Phe Pro Val Glu Cys Leu 20 25 Arg Glu Asn Ile Ala Phe Glu Leu Pro Gln Glu Phe Leu Gln Tyr Thr 40 Gln Pro Met Lys Arg Asp Ile Lys Lys Ala Phe Tyr Glu Met Ser Leu Gln Ala Phe Asn Ile Phe Ser Gln His Thr Phe Lys Tyr Trp Lys Glu Arg His Leu Lys Gln Ile Gln Ile Gly Leu Asp Gln Gln Ala Glu Tyr Leu Asn Gln Cys Leu Glu Glu Asp Glu Asn Glu Asp Met Lys 105 100 110 Glu Met Lys Glu Asn Glu Met Lys Pro Ser Glu Ala Arg Val Pro Gln 120 Leu Ser Ser Leu Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe 130 135 Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val 145 Glu Ile Arg Arg Cys Leu Tyr Tyr Phe Tyr Lys Phe Thr Ala Leu Phe

Arg Arg Lys

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<22 <22	3> D p		epti					Seq nd p								
	1> C		. (55	8)												
	0> 1 agaa		agga	ataa	ca t	_	_	aac Asn		-		-		_	_	51
_	_					_	_	cat His	_	-	_		_			99
								aac Asn 35								147
		_						atg Met			_		_	_	_	195
		-	_			_	_	ttc Phe				_				243
								ctc Leu								29 1
								caa Gln								339
								aaa Lys 115								387
								agc Ser								435
			-			_		gaa Glu	_			-	-	_	_	483

 tgg gag att gtc cga gtg gaa atc cgt cgt tct ctg tac tac ttt tac 531
Trp Glu Ile Val Arg Val Glu Ile Arg Arg Ser Leu Tyr Tyr Phe Tyr
155 160 165 170

aaa ttt acc gct ctg ttc cgt cgt aaa taatggatcc Lys Phe Thr Ala Leu Phe Arg Arg Lys 175 568

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Leu Arg His Leu Ser Ser Met Ser Asn Ser Phe Pro Val Glu Cys Leu 20 25 30

Arg Glu Asn Ile Ala Phe Glu Leu Pro Gln Glu Phe Leu Gln Tyr Thr 35 40 45

Gln Pro Met Lys Arg Asp Ile Lys Lys Ala Phe Tyr Glu Met Ser Leu 50 55 60

Gln Ala Phe Asn Ile Phe Ser Gln His Thr Phe Lys Tyr Trp Lys Glu 65 70 75 80

Arg His Leu Lys Gln Ile Gln Ile Gly Leu Asp Gln Gln Ala Glu Tyr 85 90 95

Leu Asn Gln Cys Leu Glu Glu Asp Glu Asn Glu Asp Met Lys 100 105 110

Glu Met Lys Glu Asn Glu Met Lys Pro Ser Glu Ala Arg Val Pro Gln
115 120 125

Leu Ser Ser Leu Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe 130 135 140

Glu Ile Arg Arg Ser Leu Tyr Tyr Phe Tyr Lys Phe Thr Ala Leu Phe 165 170 175

Arg Arg Lys

<21 <21	0 > 1 1 > 5 2 > D 3 > A	56 NA	icia	l Se	quen	ce									
<22 <22	3> D p		epti	on o de c				_							
	1> C	-	(546)								-	·		
cat	Met	ctg		tgt Cys 5											48
			_	aga Arg		_	_	_	_	_				_	96
				gaa Glu										ctg. Leu	144
				cct Pro											192
			_	gcc Ala					_						240
				cac His 85											288
				aac Asn											336
				atg Met											384
				agc Ser											432
				aaa Lys									Glu		480

gtc cga gtg gaa atc cgt cgt tgc ctg tac tac ttt tac aaa ttt acc 528 Val Arg Val Glu Ile Arg Arg Cys Leu Tyr Tyr Phe Tyr Lys Phe Thr 170 gct ctg ttc cgt cgt aaa taatggatcc 556 Ala Leu Phe Arg Arg Lys 180 <210> 17 <211> 182 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Human IFN-like polypeptide cDNA insert and partial pAMG21 vector sequence <400> 17 His Met Leu Asp Cys Asn Leu Leu Asn Val His Leu Arg Arg Val Thr 5 Trp Gln Asn Leu Arg His Leu Ser Ser Met Ser Asn Ser Phe Pro Val Glu Cys Leu Arg Glu Asn Ile Ala Phe Glu Leu Pro Gln Glu Phe Leu Gln Tyr Thr Gln Pro Met Lys Arg Asp Ile Lys Lys Ala Phe Tyr Glu 50 ·55 Met Ser Leu Gln Ala Phe Asn Ile Phe Ser Gln His Thr Phe Lys Tyr 70 Trp Lys Glu Arg His Leu Lys Gln Ile Gln Ile Gly Leu Asp Gln Gln Ala Glu Tyr Leu Asn Gln Cys Leu Glu Glu Asp Glu Asn Glu Asn Glu Asp Met Lys Glu Met Lys Glu Asn Glu Met Lys Pro Ser Glu Ala Arg

Val Pro Gln Leu Ser Ser Leu Glu Leu Arg Arg Tyr Phe His Arg Ile 130 135 140

Asp Asn Phe Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Ile 145 150 155 160

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Ala Leu Phe Arg Arg Lys 180

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ıD
                      5
                                          10
ıΩ
Ш
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    <211> 21
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    <400> 20
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H
<u>-</u>
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tcc		63
.210-	· · · · · · · · · · · · · · · · · · ·	
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		_
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<223>	Description of Artificial Sequence: PCR primer	
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5	-ungaugumb masacasjog cameregoog masgetouse egogoogege	-
tacctg	9	67
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cgacgat	tttc c	71

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	1967-33	
		·
	<400> 27	
	ccgcggatcc attatttacg acggaacaga gcggtaaatt tgtaaaagta gt	
	Jeggtadate tytaaagta yt	acayayaa b
	cgacggattt cc	7:
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7	<220>	
j	<223> Description of Artificial Sequence: PCR primer	
]	2103-87	
Ü		
	<400> 28	
ā	aaggagcata tgctggactg taacctgctg aacgttcac	39
₩ F		3.
٥	<210> 29	
	<211> 20	
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	10107	merrae bequence	
	<220>		
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=		tegae teateaatte atgttgagta gtttg	
٥	acgcg	· · · · · · · · · · · · · · · · · · ·	
		,	
Ļ	<210>	33	
ij	<211>	39	
Ō	<212>	DNA	
	<213>	Artificial Sequence	
3	-220-		
	<220>		
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Ō		1090-37	
♣ .	<400>	33	
_		aaaaa geggeegete atcaatteat gttgagtag	
		3 - 3 3	•
<u>.</u>			
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	\2237	1954-45	THICT
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1954-46

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